atgagggcccctgctcagatttttggattcttggtcaggagacgttgt tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca ACTAGTCGACATGAGGGCCCCTGCTCAGTTTTTTGGCTTCTTG-3' C AA MKV4 PRIMER agaaatgagaccgtctattcagttcctggggctcttgttgttctggcttcatgg tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc L L F [M - R P]S Ι Q F L G L LEADER tgctcagtgtgacatccagatgacacagtctccatcctcactgtctgcatctct acqaqtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga S L C][D Ι S Ρ L S FR1 gggaggcaaagtcaccatcacttgcaagacaagccaagacattaacaagtatat 157 --ccctccgtttcagtggtagtgaacgttctgttcggttctgtaattgttcatata G G K V Ι Cl[K S D Ι Κ Y Μ CDR1 ggcttggtaccaacacaagcctggaaaacgtcctaggctgctcatacattacac ccqaaccatggttgttcggaccttttgcaggatccgacgagtatgtaatgtg G K Ι H][Y A] [W K Ρ R Ρ R \mathbf{L} L FR2 atctgcattacagccaggcatcccatcaaggttcagtggaagtgggtctgggag 265 -tagacgtaatgtcggtccgtagggtagttccaagtcaccttcacccagaccctc Α Ρ S R F S G S G R L 0 P][G I CDR2

FIG. 1-1.



tctaataaggaagttgtagtcgttggacctcggacttctataacgttga D Y S F N I S N L E P E D I A T FR3 ttgtctacagtatgataatctgtggacgttcggtggaggcaccaagctg 373	tatta
FR3 ttgtctacagtatgataatctgtggacgttcggtggaggcaccaagctg 373	ataat
aacagatgtcatactattagacacctgcaagccacctccgtggttcgaccctgll Q Y D N L W T][F G G G T K L CDR3 FR4	Y Y
aacagatgtcatactattagacacctgcaagccacctccgtggttcgacctglacctccgtggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaagccacctccgtggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaggttcgacctgcaagccacctccgtggttcgacctgcaggttcaggttcgacctgcaggttc	gaaat
CDR3 FR4	cttta
MOUSE KAPPA PRI	E I
3'-GTAGAAGGGTAGGTG	GCCCT
caaacgggctgatgctgcaccaactgtatccatcttcccaccatccac	
gtttgcccgactacgacgtggttgacataggtagaagggtggtaggtg	ggccct
K]	
AGG-5' tcc 481 agg	

FIG. 1-2.

atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg tactttacgtcgacccagtacaagaaggactaccgtcaccaatgtccc ACTAGTCGACATGAAATGCAGCTGGGTCATCTTCTTC-3' MHV1 PRIMER M K С S W V Μ F F L Μ Α G LEADER gtcaattcagaggttcagctgcagcagtctggggcagagcttgtgaagccaggg cagttaagtctccaagtcgacgtcgtcagaccccgtctcgaacacttcggtccc V N SIE V 0 L Q S G Α Ε L K V Ρ G FR1 gcctcagtcaagttgtcctgcacagcttctggcttcaacattaaagacacctat cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata S K L S C T Α S G F N Y K) [D CDR1 atacactgtgtgaagcagaggcctgaacagggcctggagtggattggaaggatt 157 tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa Ι H)[C K R P Ε 0 G L Ε W G][R FR2 gatcctgcgaatggttatactaaatatgacccgaagttccagggcaaggccact 211 ctaggacgcttaccaatatgatttatactgggcttcm=ggtcccgttccggtga Ρ D Ν G Y K Y D P Κ G][K F CDR2 ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca tattgtcgactgtgtaggaggttgtgtcggatggacgtcgagtcgtcggactgt Ι S Y L L 0 S S T FR3 FIG. 2-1.



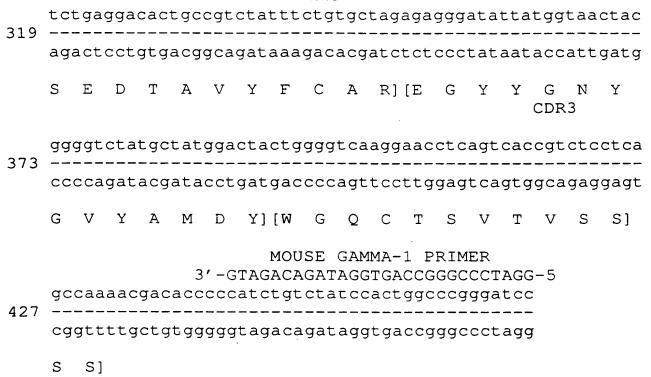
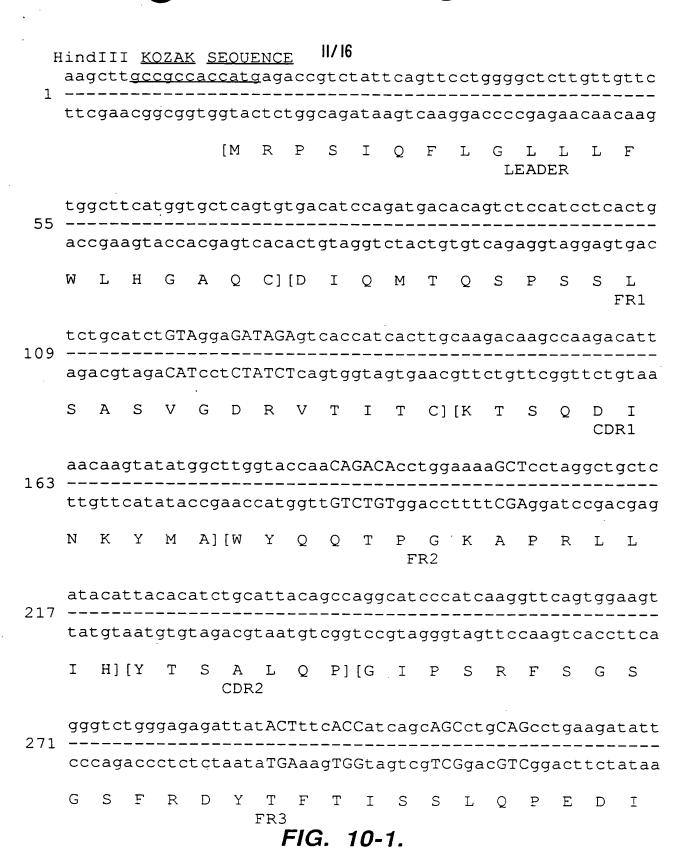
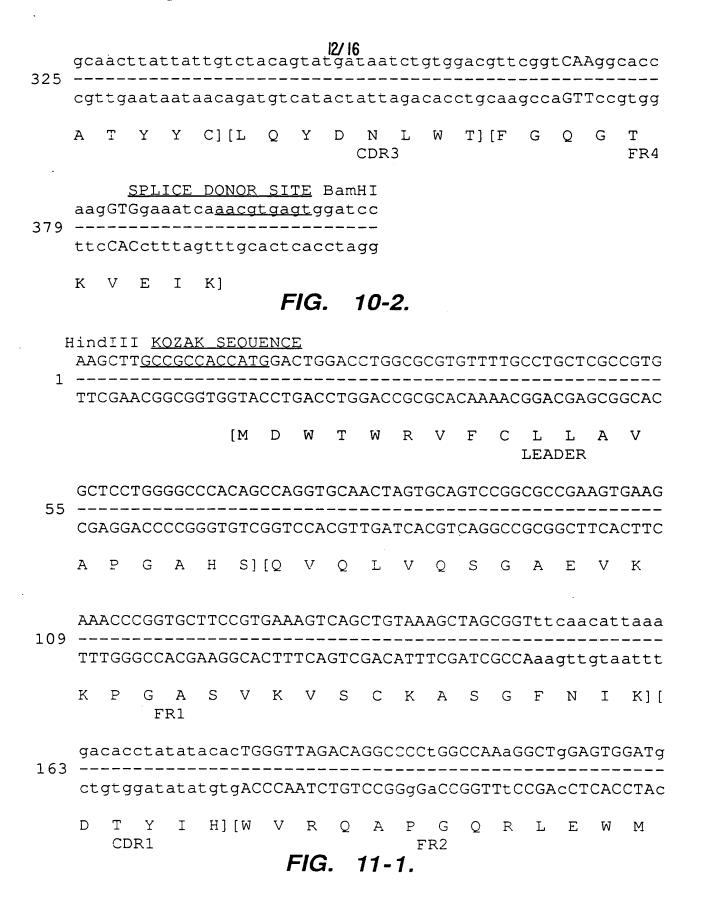


FIG. 2-2.









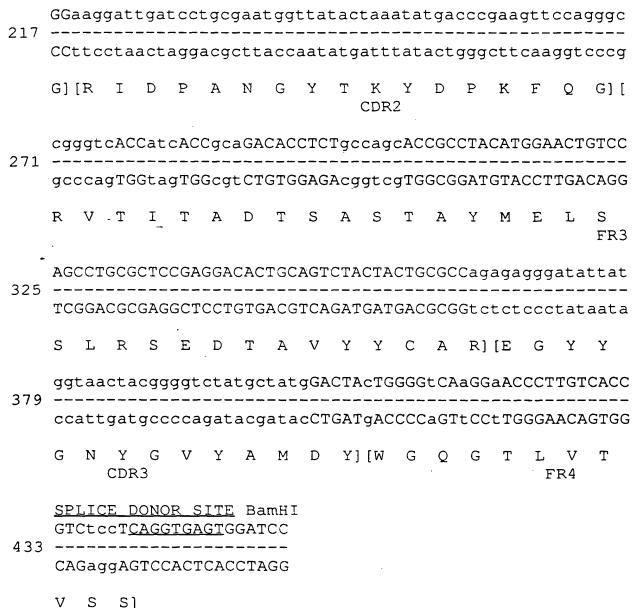


FIG. 11-2.